

**INFORMATION  
DISCLOSURE  
STATEMENT**

Atty. Docket No.: 6263.N

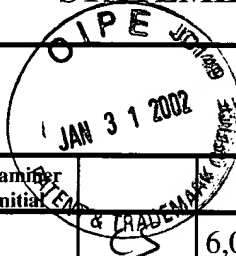
Serial No.: 09/847,670

Applicant(s): Finzel et al.

Confirmation No.: 4815

Filing Date: May 2, 2001

Group: 1645-1631


**U.S. PATENT DOCUMENTS**

Examiner Initial	Document Number	Date	Name	Class	Subclass	Filing Date If Appropriate
CS	6,093,573	07/25/00	Beamer et al.	436	86	

**FOREIGN PATENT DOCUMENTS**

Examiner Initial	Document Number	Date	Country	Class	Subclass	Translation
CS	WO 93/02209	02/04/93	PCT wipo			
	WO 97/15588	05/01/97	PCT wipo			
	WO 99/36422	07/22/99	PCT wipo			

**OTHER DOCUMENTS (Including Authors, Title, Date, Pertinent Papers, etc.)**

Examiner Initial	Document Description
CS	Bartlett et al., "CAVEAT: A Program to Facilitate the Structure-derived Design of Biologically Active Molecules," Molecular Recognition: Chemical and Biological Problems, <i>Royal Society of Chemistry</i> , Special Pub. No. 78:182-196 (1989).
	Blundell, T.L. and Johnson, N.L., Protein Crystallography, Academic Press, title page, publication page, and table of contents only (8 pages total) (1976).
	Böhm, "The computer program LUDI: a new method for the de novo design of enzyme inhibitors," <i>J. Comput. Aided Mol. Des.</i> 1992;6(1):61-78.
	Brünger, "Crystallographic refinement by simulated annealing. Application to a 2.8 Å resolution structure of aspartate aminotransferase," <i>J. Mol. Biol.</i> 1988; 203(3):803-16.
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	Brünger, "Free R value: a novel statistical quantity for assessing the accuracy of crystal structures," <i>Nature.</i> 1992;355:472-5.

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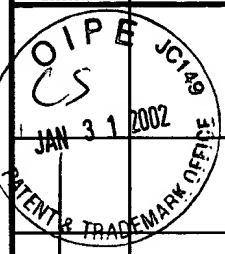
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CS	Brünger, "A system for crystallography and NMR," X-PLOR Manual, Version 3.1, Yale University Press, New Haven, CT (1992) (title page, publication page, and table of contents only (13 pages)).
	Cho et al., "Crystal structure of RNA helicase from genotype 1b hepatitis C virus. A feasible mechanism of unwinding duplex RNA," <i>J. Biol. Chem.</i> 1998; 273(24):15045-52.
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	Gorbalenya et al., "Helicases: amino acid sequence comparisons and structure-function relationships," <i>Current Opin. in Struct. Biol.</i> 1993;3:419-429.
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	Hendrickson et al., "Selenomethionyl proteins produced for analysis by multiwavelength anomalous diffraction (MAD): a vehicle for direct determination of three-dimensional structure," <i>EMBO J.</i> 1990;9(5):1665-72.
	Houghton, M., in <i>Fields virology</i> , eds., Fields et al., Raven Press, New York, NY, Third Ed., Vol. 1, pp. 1035-1058 (1996).
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Lauri et al., "CAVEAT: a program to facilitate the design of organic molecules," <i>J. Comput. Aided Mol. Des.</i> 1994;8(1):51-66.	
✓	Martin, "3D database searching in drug design," <i>J. Med. Chem.</i> 1992; 35(12):2145-54. Review.

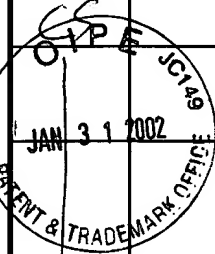
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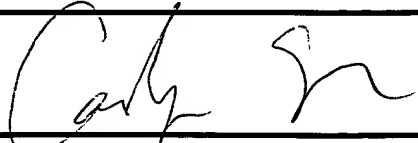
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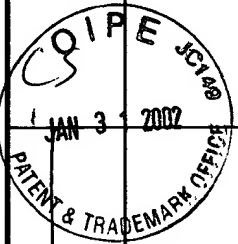
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	Matthews, "Solvent content of protein crystals," <i>J. Mol. Biol.</i> 1968;33(2):491-7.
	Meng et al., "Automated Docking with Grid-Based Energy Evaluation," <i>J. Comp. Chem.</i> , 1992;13(4):505-524.
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✓	Tong et al., "The locked rotation function," <i>Acta Crystallogr.</i> 1990;A46:783-92.

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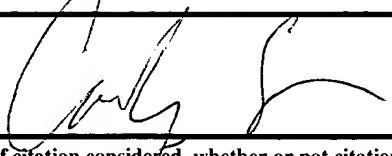
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	Walker et al., "Distantly related sequences in the alpha- and beta-subunits of ATP synthase, myosin, kinases and other ATP-requiring enzymes and a common nucleotide binding fold," <i>EMBO J.</i> 1982;1(8):945-51.
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	Yao et al., "Structure of the hepatitis C virus RNA helicase domain," <i>Nat. Struct. Biol.</i> 1997;4(6):463-7.

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